



phylogenetic tree. Results confirmed that R1101 is a member of *R. rhodochrous* and is phylogenetically distant from *R. equi*.

We used a BLASTP search to determine the similarity of predicted R1101 proteins to homologous proteins from *R. equi* 103S, *R. erythropolis* (PR4 and SK121), and *R. pyridinivorans* (AK37 and BKS6-46) (Figure, panel C, Appendix, [wwwnc.cdc.gov/EID/article/18/11/12-0818-F1.htm](http://wwwnc.cdc.gov/EID/article/18/11/12-0818-F1.htm)). These data indicate that R1101 is highly similar to but distinct from *R. pyridinivorans* and *R. rhodochrous* at the protein sequence level and is more distantly related to *R. equi*.

Each R1101 protein  $\geq 1$  database blast hit with an E-value  $\leq 1 \times 10^{-10}$  was assigned a best match to another species on the basis of its bit score. Consistent with the 16S rRNA-based phylogenetic analysis,  $>92\%$  of the R1101 proteins showed greatest similarity to a protein from *R. pyridinivorans*, *R. rhodochrous*, or *Rhodococcus* sp. R04. However, 120 proteins (3%) have highest homology to their counterparts in the pathogen *R. equi*; 10 of these are unique to R1101 and *R. equi*. Furthermore, genes with the greatest similarity to *R. equi* are not randomly distributed throughout the R1101 genome.

We calculated the probability of observing groups of adjacent R1101 genes that are most similar to *R. equi* and observed 1 cluster of 5 adjacent genes ( $p = 2.33 \times 10^{-8}$ ), 2 groups of 6 adjacent genes ( $p = 6.75 \times 10^{-10}$ ), and 2 blocks of 7 contiguous genes ( $p = 1.94 \times 10^{-11}$ ). Nucleotide BLAST analysis showed that R1101 sequence contigs 604, 456, 139, and 610 align to nt 4454241–4469589 of the *R. equi* 103S chromosome, with  $>97\%$  identity at the DNA level. The 12 proteins wholly or partially encoded within this 15.3-kb region show  $>99\%$  identity at the amino acid level with their R1101 orthologs. Among them, contig 139 encodes a cluster of 7 consecutive proteins with high homology to *R. equi*; this portion of the R1101 ge-

nome is likely to have been acquired from *R. equi* through horizontal gene transfer. R1101 may have acquired clusters of virulence-related genes, such as those crucial iron-uptake proteins (9), from the phylogenetically distant species *R. equi*.

In conclusion, infections caused by non-*equi* *Rhodococcus* spp. are rare, especially in immunocompetent patients, but may represent an emerging threat. Specialized diagnostics such as genome sequencing may be needed to accurately identify these pathogens.

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